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Figure 1a

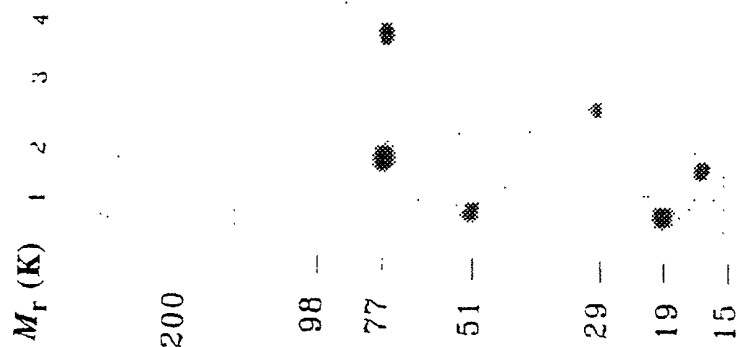
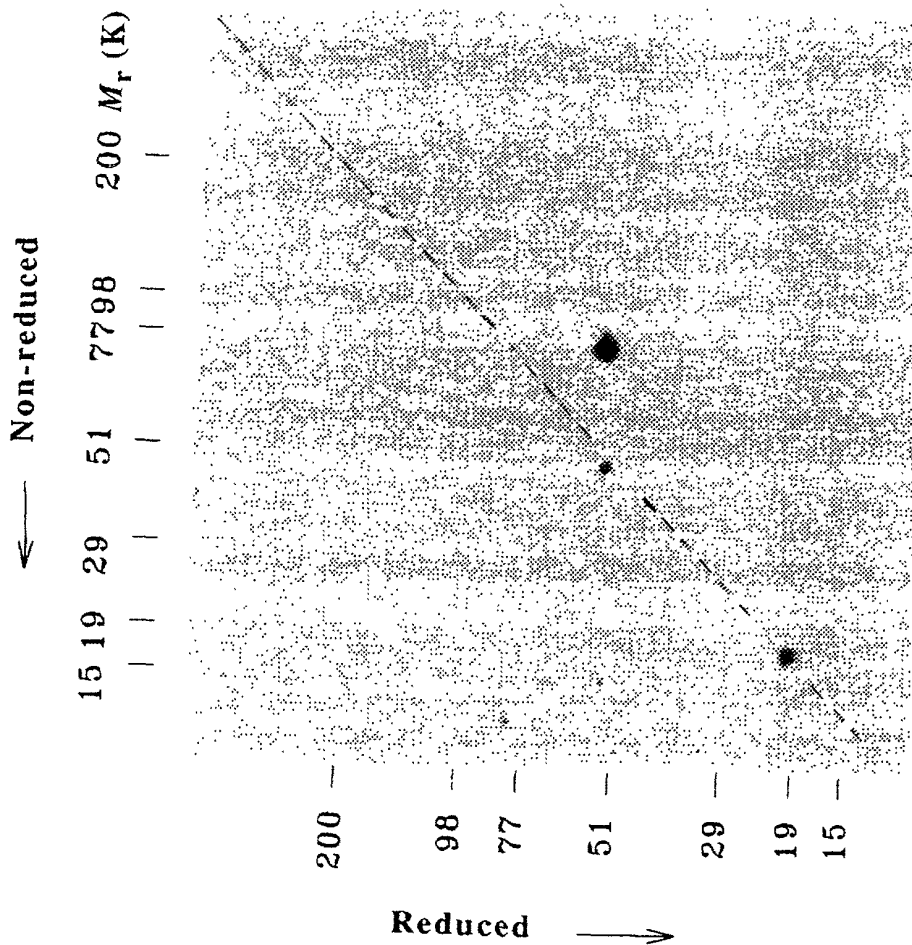


Figure 1b

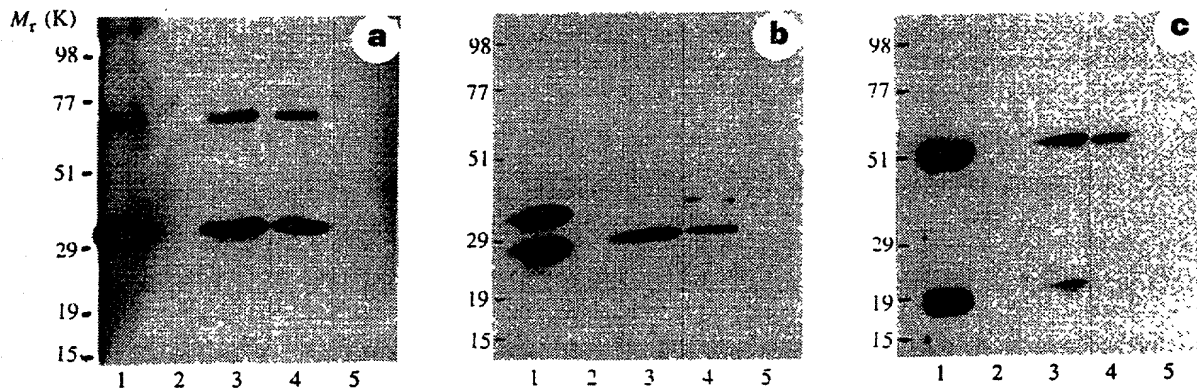


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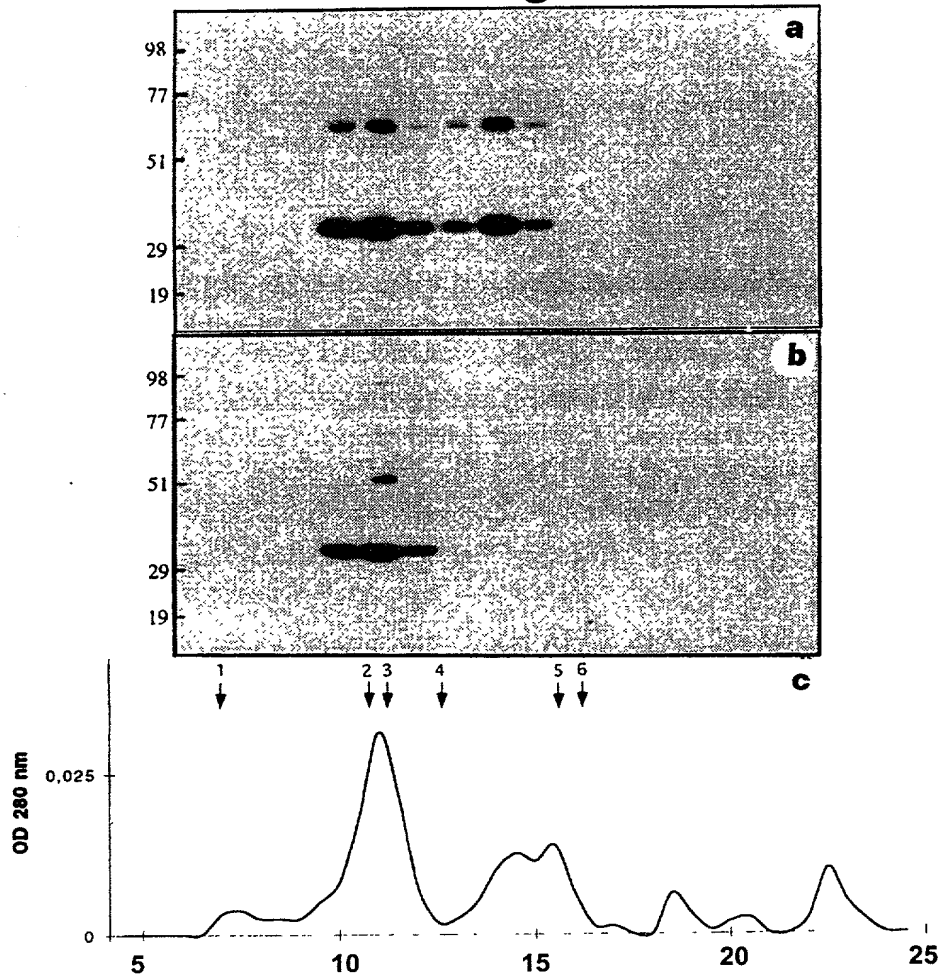
Figure 2

	Clr/Clis →		
MAASP-2	TPLGPKWPEPVFGRLASPGFPGEYANDQERRWLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLGGQESTDTERAPGKDT	90	
MAASP-1	HTVELNMMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETTDTEQTPGQEV	87	
Clr	SIPIPQKLFGEVTSPLFPKPYNNFETTTVITVPTGYRVKLVFQQFDLEPSEGCFYDYVKISADKKSLGRFGQGLGSPLGNPPGKKE	87	
Clis	EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLYFTHLDIELSENCAIDSVQIISGDTTEEGRLCGQRSSNNPHSPIVEE	83	
	* * * * *		
	ECF →		
MAASP-2	FYSLGSSLDITFRSDYSNEKP FTGFEEAFYAEDIDECQ VAPGEA PTGDHHCNHLGGFYCSERAGYVLRNKRRTSALCS	170	
MAASP-1	VLSPGSFMSTIFRSDFSNEER FTGFDAHYMAVDVDECK EREDEE LSCDHYCHNYIGGYVCSRFGYILHTDNRTSRVES	167	
Clr	FMSQGNKMLLTFTHTDFSNEENGTFIMFYKGFLLAYQAVDLDECSASRSKSGEEDPQPOQOHLCHNYVGGYFCSRPGYELQEDRHSQAECS	177	
Clis	FQVPYNKLQVIFKSDFSNEER FTGFAAYYVATDINECT DFVD VPCSHFENNFIGGYFCSRPPEYFLHDDMKNGVNCIS	161	
	* * * * *		
	- Clr/Clis →		
MAASP-2	GQVFTQSRGELSSPEYPRPYKLSSTYSSISLEEGFSVILDFV ESFDVET HPETLCOPYDFLKIQTDRREHGPFQKTLPHR IETKS	256	
MAASP-1	DNLFTQRTGVITSPDPNPNPKSSECLYTIELEEGFMVNLOFE DIFDIED HPEVDPYDYIKIKVGPVKLGPFQCEKAPEP ISTQS	253	
Clr	SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL EPFDIDD HQQVHCOPYDQLQIYANGKNIGEFQKQRPDP LDTSS	263	
Clis	GDVFTALIGEIASPNYPKPYNSRCEYQIRLEKGFQVVTLRRREDFVEAADSAGNC LDSLVFVAGDRQFGPYCGHGFPGPLNIETKS	250	
	* * * * *		
	CCP-1 →		
MAASP-2	NTVTITFTVDES DHTGWKIHYTSTAQCPYPMAPPN GHVSPVQAKYILKDSFSIFCETGYELLQGHLPKLSFTAVCQKDGSDWRMPA	345	
MAASP-1	HSVLILFHS DNGENRGWRLSYRAAGNECPQLQPPVH GKIEPSQAKYFPKQVLSVETGYKVLKDNVEMDTFQIECLKDGTSNKIPT	342	
Clr	NAVDLLFFTDDES DSGRWKLRYTEIIKCPQPKLTDEFTIIQNLQPYQFRDYFIATCKQGYQLIEGNQVLSFTAVCQDDGTWHRAMPR	353	
Clis	NALDIIFQD TDLTGQKKGWKLRYHGDMPKPKEDTPN SVWEPAKAKYVFRDVOITCLDGFVEVGRVGATSFYSTCQSNKWSNKLK	338	
	* * * * *		
	CCP-2 →		
MAASP-2	ESIVDCGPPDDLPSGRVEYITGPGVTTYKAVIQYSCSEETFTYM KVNDGKVCCEADGEFTSSKGEKSLPVCPEVCGLS ARTT	426	
MAASP-1	CKIVDCRAPGELEHGLITFSTRNNLTYYKSEIKYSCQEPYYKML NNNTGIYTCSAQGVMMNKVLGRSLPTCLPVCGLPKFSRKL	426	
Clr	CKIKDGGQPRNLPNGDFRYTTTGMVNTYKARIQYCHPEYKQTRAGSRESEQGVYTTCTAAGIWNKQKGEKIPRCLPVGKPVNVEEQ	443	
Clis	QOPVDGIPES IENGKVE DPESTLFGSVIRYTCPEPYTYME NGGGGEYHCAGNGSWVNEVLGPPLPKCPVPGVPREPFE	419	
	* * * * *		
	serine protease →		
MAASP-2	GGRIYGGQKAKPGDFPWQVLILGGTTA AGALLYDNWVLTAAH AVVEQKHDA SLDIRMGTLKRLSPHYTQAWSEAVFIHEG	507	
MAASP-1	MARIFNGRPAQKGTTPWIAMLSHLNGQPFQGGSLGSSWIVTAACHLQSLDPKDPTRLRSDLLSPSD FKILGKHWRLSRSDENEQHLG	515	
Clr	RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSNASLDVFLGHTNVEELMKLGNHP IRRV	523	
Clis	KQRIIGGSDADIKNFPWQVFPDNPWA GGALINEYWVLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG	498	
	* * * * *		
	◇		
MAASP-2	YTHDAG FDNDIALIKLNKVVINSNITPICLPKREAESFMRTDDIGTASGWGLTQRGFLARNLMYVDIPVDHOKCTAAYEK	589	
MAASP-1	VKHTTLHPKYDPTNTFENDVALVELLESPLNNAFVMPILP EGPQEGAMVIVSGWGKQFLQRFPETLMEIEIPVDHSTCKAY	599	
Clr	SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPIQLP DNDTFYDLGLMGYVSGFGVMEEK IAHDRLFRVRLPVANPOACEN WLR	608	
Clis	WKLLEV PEGRTN FDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKEKVKVE	586	
	* * * * *		
	◇		
MAASP-2	PPYPRG SVTANMLCAGLES GKGDSGRGSGGALVFLDS ETERWFVGIVSWGSMNCEAGQYGVYTKVINIYIPWIENIISDF	671	
MAASP-1	APLKK KVTRDMICAGEKEGGKDAQSGSGGPMVTLNR ERGQWLVGTVSWGD DCGKKDRYGVYSYIHHNKDWIQRVTGVRN	680	
Clr	GKNRMD VFSQNMFCAGHPSLKQDAQCGDSGGVFAVRDP NTRDWATGIVSWG GCSRG YGFYTKVLNVYDWMKEMEBED	688	
Clis	KPTADAEAYVFTNMICAGGEK GMDSCKGDSGGAFVQDPNDKTKFYAAGLVSWG QCGT YGLYTRVKNYVDWMKTMQENSTPRED	673	
	* * * * *		

### 3/6 Figure 3a



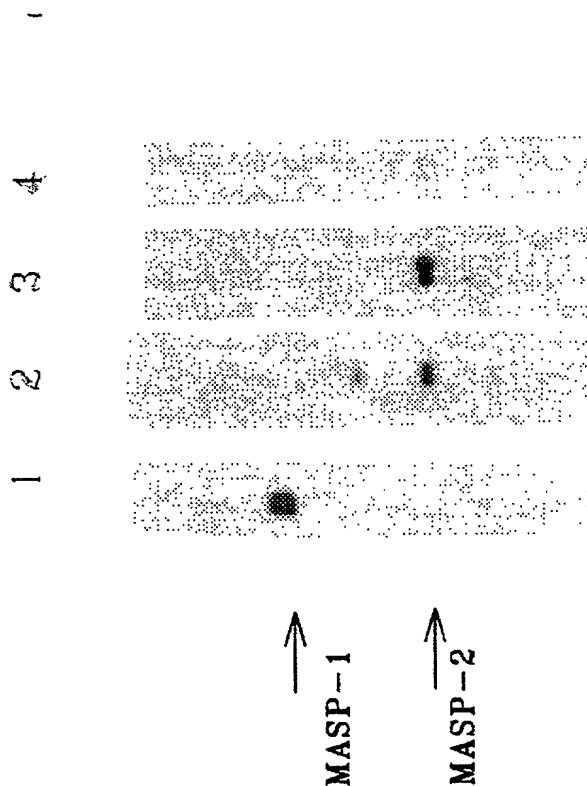
### Figure 3b



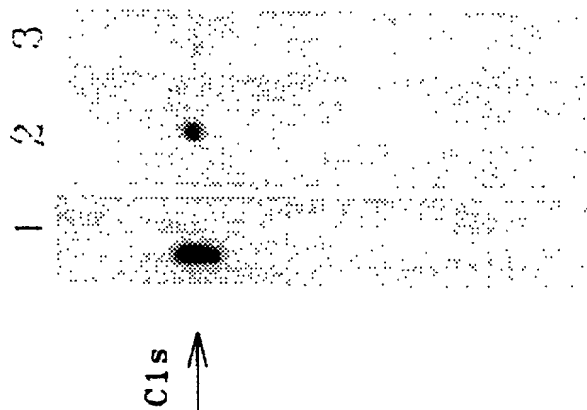
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Figure 4

Blot of MBL preparation

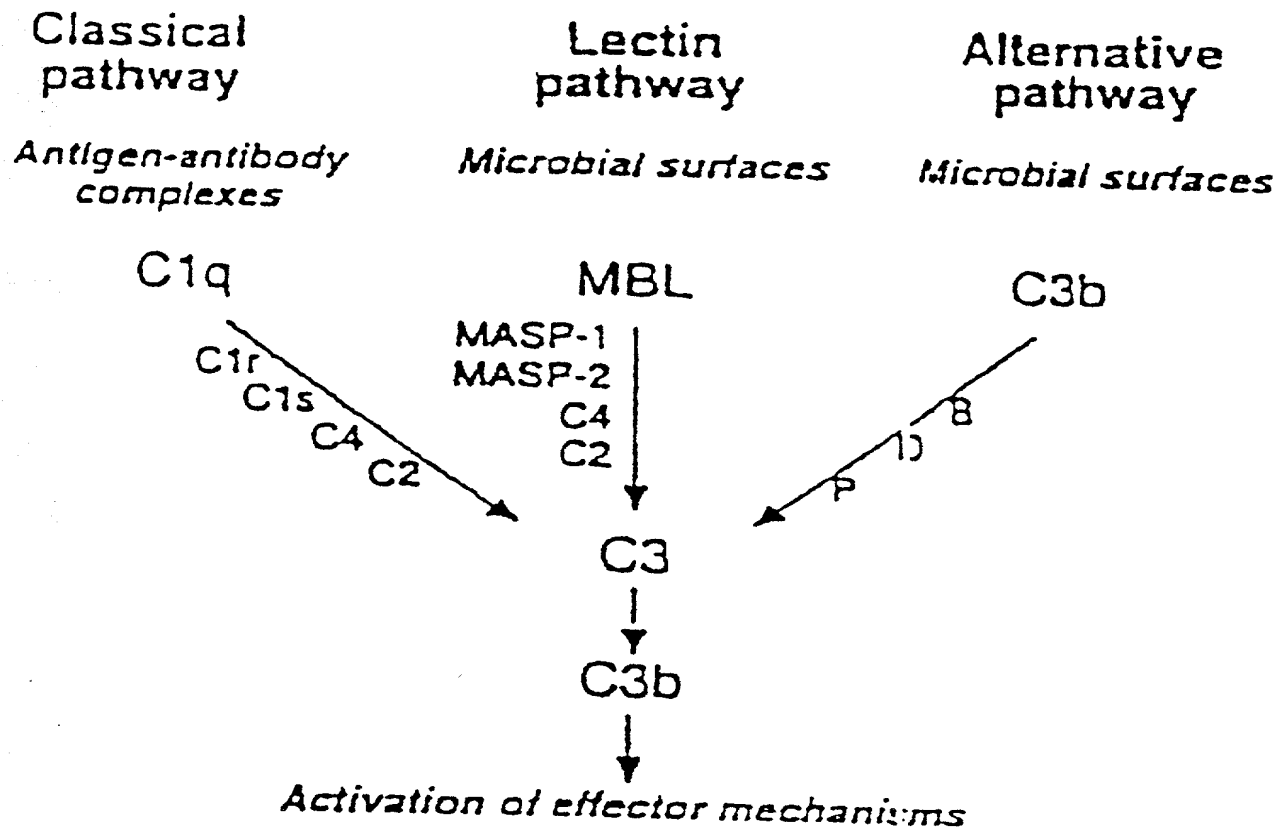


Blot of C1



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Figure 5



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Figure 6

+1  
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M R L L T L L G L L C G S V A T P L G P K 6  
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W P E P V F G R L A S P G F P G E Y A N D O E R R W T L T A P P G Y 40  
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R L R L Y F T H F D L E L S H L C E Y D F V K L S S G A K V L A T 73  
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L C G Q E S T D T E R A P G K D T F Y S L G S S L D I T F R S D Y 106  
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S N E K P P T G F E A F Y A A E D I D E C Q V I P G E A P T C D H H 140  
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C H N H L G G F Y C S C R A G Y V L H R N K R T C S A L C S G Q V 173  
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